This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3   (1)   General Information:
4
5   (i) APPLICANT: Grotendorst, Gary R.
6   Bradham Jr., Douglas M.,
7
8   (ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
9
10   (iii) NUMBER OF SEQUENCES: 2
11
12   (iv) CORRESPONDENCE ADDRESS:
13   (A) ADDRESSEE: Spensley Horn Jubas & Lubitz
14   (B) STREET: 4225 Executive Square, Suite 1400
15   (C) CITY: La Jolla
16   (D) STATE: CA
17   (E) COUNTRY: US
18   (F) ZIP: 92037
19
20   (v) COMPUTER READABLE FORM:
21   (A) MEDIUM TYPE: Floppy disk
22   (B) COMPUTER: IBM PC compatible
23   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24   (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
25
26   (vi) CURRENT APPLICATION DATA:
27   (A) APPLICATION NUMBER: US 08/386,680
28   (B) FILING DATE: 10-FEB-1995
29   (C) CLASSIFICATION: 435
30
31   (vii) PRIOR APPLICATION DATA:
32   (A) APPLICATION NUMBER: US/08/167,628
33   (B) FILING DATE:
34
35   (A) APPLICATION NUMBER: US/07/752,427
36   (B) FILING DATE:
37
38   (viii) ATTORNEY/AGENT INFORMATION:
39   (A) NAME: Wetherell, Jr. Ph.D., John W.
40   (B) REGISTRATION NUMBER: 31,678
41   (C) REFERENCE/DOCKET NUMBER: PD-1294
42
43   (ix) TELECOMMUNICATION INFORMATION:
44   (A) TELEPHONE: 619-455-5100
45   (B) TELEFAX: 619-455-5110
46

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47
48      (2) INFORMATION FOR SEQ ID NO:1:
49
50          (i) SEQUENCE CHARACTERISTICS:
51              (A) LENGTH: 2075 base pairs
52              (B) TYPE: nucleic acid
53              (C) STRANDEDNESS: single
54              (D) TOPOLOGY: linear
55
56         (ii) MOLECULE TYPE: cDNA
57
58
59        (vii) IMMEDIATE SOURCE:
60              (B) CLONE: DB60R32
61
62         (ix) FEATURE:
63              (A) NAME/KEY: CDS
64              (B) LOCATION: 130..1177
65
66
67         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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71 CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA       120
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73 GTGCCAACC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC TTC          168
74            Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe
75             1               5                  10
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77 GTG GTC CTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG AAC TGC       216
78 Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys
79    15              20                 25
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81 AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CCG GCG       264
82 Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala
83    30                 35                 40                 45
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85 GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC TGC GCC       312
86 Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala
87             50                 55                 60
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89 AAG CAG CTG GGC GAG CTG TGC ACC GAG CGC GAC CCC TGC GAC CCG CAC       360
90 Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His
91             65                 70                 75
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93 AAG GGC CTC TTC TGT GAC TTC GGC TCC CCG GCC AAC CGC AAG ATC GGC       408
94 Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly
95             80                 85                 90
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97 GTG TGC ACC GCC AAA GAT GGT GCT CCC TGC ATC TTC GGT GGT ACG GTG       456
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INPUT SET: S14073.raw

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105   TGC CTG GAC GGG GCG GTG GGC TGC ATG CCC CTG TGC AGC ATG GAC GTT      552
106   Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val
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109   CGT CTG CCC AGC CCT GAC TGC CCC TTC CCG AGG AGG GTC AAG CTG CCC      600
110   Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro
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114   Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr
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117   GTG GTT GGG CCT GCC CTC GCG GCT TAC CGA CTG GAA GAC ACG TTT GGC      696
118   Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly
119               175                 180                 185
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121   CCA GAC CCA ACT ATG ATT AGA GCC AAC TGC CTG GTC CAG ACC ACA GAG      744
122   Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu
123   190                 195                 200                 205
124
125   TGG AGC GCC TGT TCC AAG ACC TGT GGG ATG GGC ATC TCC ACC CGG GTT      792
126   Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val
127               210                 215                 220
128
129   ACC AAT GAC AAC GCC TCC TGC AGG CTA GAG AAG CAG AGC CGC CTG TGC      840
130   Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys
131               225                 230                 235
132
133   ATG GTC AGG CCT TGC GAA GCT GAC CTG GAA GAG AAC ATT AAG AAG GGC      888
134   Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly
135               240                 245                 250
136
137   AAA AAG TGC ATC CGT ACT CCC AAA ATC TCC AAG CCT ATC AAG TTT GAG      936
138   Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu
139       255                 260                 265
140
141   CTT TCT GGC TGC ACC AGC ATG AAG ACA TAC CGA GCT AAA TTC TGT GGA      984
142   Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly
143   270                 275                 280                 285
144
145   GTA TGT ACC GAC GGC CGA TGC TGC ACC CCC CAC AGA ACC ACC ACC CTG      1032
146   Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu
147               290                 295                 300
148
149   CCG GTG GAG TTC AAG TGC CCT GAC GGC GAG GTC ATG AAG AAG AAC ATG      1080
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INPUT SET: S14073.raw

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157    GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T     1177
158    Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
159            335                 340                 345
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161    GAAGCCAGAG AGTGAGAGAC ATTAACTCAT TAGACTGGAA CTTGAACTGA TTCACATCTC     1237
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163    ATTTTTCCGT AAAAATGATT TCAGTAGCAC AAGTTATTTA AATCTGTTTT TCTAACTGGG     1297
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165    GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC     1357
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167    CCAGACACTG GTTTGAAGAA TGTTAAGACT TGACAGTGGA ACTACATTAG TACACAGCAC     1417
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169    CAGAATGTAT ATTAAGGTGT GGCTTTAGGA GCAGTGGGAG GGTACCGGCC CGGTTAGTAT     1477
170
171    CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATTT GAAGTGTAAT TGAGAAGGAA     1537
172
173    AATTTTAGCG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC     1597
174
175    CAGCCATCAA GAGACTGAGT CAAGTTGTTC CTTAAGTCAG AACAGCAGAC TCAGCTCTGA     1657
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177    CATTCTGATT CGAATGACAC TGTTCAGGAA TCGGAATCCT GTCGATTAGA CTGGACAGCT     1717
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179    TGTGGCAAGT GAATTTGCCT GTAACAAGCC AGATTTTTTA AAATTTATAT TGTAAATATT     1777
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181    GTGTGTGTGT GTGTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTTAA     1837
182
183    AGTTGTTTGT GCCTTTTTAT TTTTGTTTTT AATGCTTTGA TATTTCAATG TTAGCCTCAA     1897
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185    TTTCTGAACA CCATAGGTAG AATGTAAAGC TTGTCTGATC GTTCAAAGCA TGAAATGGAT     1957
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187    ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCCGT CAAAACAGAT TGTTTGCAAA     2017
188
189    GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCACG       2075
190
191
192    (2) INFORMATION FOR SEQ ID NO:2:
193
194            (i) SEQUENCE CHARACTERISTICS:
195                  (A) LENGTH: 349 amino acids
196                  (B) TYPE: amino acid
197                  (D) TOPOLOGY: linear
198
199            (ii) MOLECULE TYPE: protein
200
201            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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205
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206   Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
207               20              25                  30
208
209   Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
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211
212   Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
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214
215   Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
216     65              70                  75                      80
217
218   Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
219               85                  90                      95
220
221   Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
222           100             105                 110
223
224   Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
225           115             120                 125
226
227   Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
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230   Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
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232
233   Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
234               165                 170                     175
235
236   Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
237           180                 185                 190
238
239   Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
240           195                 200                 205
241
242   Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
243           210             215                 220
244
245   Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
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247
248   Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
249               245                 250                     255
250
251   Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
252           260                 265                 270
253
254   Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
255           275                 280                 285
256
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258           290                 295                 300
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/386,680*

INPUT SET: S14073.raw

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